

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LEHRER, ROBERT I.  
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KOKRYAKOV, VLADIMIR N.

(ii) TITLE OF INVENTION: PROTEGRINS

(iii) NUMBER OF SEQUENCES: 76

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/128,345  
(B) FILING DATE: 03-AUG-1998  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Coruzzi, Laura, A.  
(B) REGISTRATION NUMBER: 30,742  
(C) REFERENCE/DOCKET NUMBER: 8067-0054-999

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 691 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG	48
Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp	
1 5 10 15	
CTT CTG CTG CTG GCA CTC GTG GTG CCC TCG GCC AGC GCC CAG GCC CTC	96
Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu	
20 25 30	
AGC TAC AGG GAG GCC GTG CTT CGT GCT GTG GAT CGC CTC AAC GAG CAG	144
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln	
35 40 45	
TCC TCG GAA GCT AAT CTC TAC CGC CTC CTG GAG CTG GAC CAG CCG CCC	192
Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro	
50 55 60	
AAG GCC GAC GAG GAC CCG GGC ACC CCG AAA CCT GTG AGC TTC ACG GTG	240
Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val	
65 70 75 80	
AAG GAG ACT GTG TGT CCC AGG CCG ACC CGG CAG CCC CCG GAG CTG TGT	288
Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys	
85 90 95	
GAC TTC AAG GAG AAC GGG CGG GTG AAA CAG TGT GTG GGG ACA GTC ACC	336
Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr	
100 105 110	
CTG GAT CAG ATC AAG GAC CCG CTC GAC ATC ACC TGC AAT GAG GTT CAA	384
Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln	
115 120 125	
GGT GTC AGG GGA GGT CGC CTG TGC TAT TGT AGG CGT AGG TTC TGC GTC	432
Gly Val Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val	
130 135 140	
TGT GTC GGA CGA GGA TGA CGGTTGCGAC GGCAGGCTTT CCCTCCCCCA	480
Cys Val Gly Arg Gly *	
145 150	
ATTTTCCCGG GGCCAGGTTT CCGTCCCCCA ATTTTTCCGC CTCCACCTTT CCGGCCCGCA	540
CCATTGGTC CACCAAGGTT CCCTGGTAGA CGGTGAAGGA TTTGCAGGCA ACTCACCCAG	600
AAGGCCTTTC GGTACATTAA AATCCCAGCA AGGAGACCTA AGCATCTGCT TTGCCAGGC	660
CCGCATCTGT CAAATAAATT CTTGTGAAAC C	691

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 150 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp  
1 5 10 15

Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu  
20 25 30

Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln  
35 40 45

Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro  
50 55 60

Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val  
65 70 75 80

Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys  
85 90 95

Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr  
100 105 110

Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln  
115 120 125

Gly Val Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val  
130 135 140

Cys Val Gly Arg Gly \*  
145 150

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 691 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG  
Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp

48

155	160	165	
CTT CTG CTG CTG GCA CTC GTG GTG CCC TCG GCC AGC GCC CAG GCC CTC Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu 170	175	180	96
AGC TAC AGG GAG GCC GTG CTT CGT GCT GTG GAT CGC CTC AAC GAG CAG Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln 185	190	195	144
TCC TCG GAA GCT AAT CTC TAC CGC CTC CTG GAG CTG GAC CAG CCG CCC Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro 200	205	210	192
AAG GCC GAC GAG GAC CCG GGC ACC CCG AAA CCT GTG AGC TTC ACG GTG Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val 215	220	225	240
AAG GAG ACT GTG TGT CCC AGG CCG ACC CGG CAG CCC CCG GAG CTG TGT Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys 235	240	245	288
GAC TTC AAG GAG AAC GGG CGG GTG AAA CAG TGT GTG GGG ACA GTC ACC Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr 250	255	260	336
CTG GAT CAG ATC AAG GAC CCG CTC GAC ATC ACC TGC AAT GAG GTT CAA Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln 265	270	275	384
GGT GTC AGG GGA GGT CGC CTG TGC TAT TGT AGG CGT AGG TTC TGC ATC Gly Val Arg Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Ile 280	285	290	432
TGT GTC GGA TGA GGATGACGGT TGCGACGGCA GGCTTCCCT CCCCCAATT Cys Val Gly *			484
295			
TCCCCGGGCC AGGTTCCGT CCCCCAATT TTCCGCCTCC ACCTTCCGG CCCGCACCAT			544
TCGGTCCACC AAGGTTCCCT GGTAGACGGA GAGGGATTG CAGGCAACTC ACCCAGAAGG			604
CCTTTCGGTA CATTAATTCATC CCAGCAAGGA GACCTAAGCA TCTGCTTGC CCAGGCCGC			664
ATCTGTCAA TAAATTCTTG TGAAACC			691

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 148 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp  
1 5 10 15

Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu  
20 25 30

Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln  
35 40 45

Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro  
50 55 60

Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val  
65 70 75 80

Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys  
85 90 95

Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr  
100 105 110

Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln  
115 120 125

Gly Val Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Ile  
130 135 140

Cys Val Gly \*

145

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG 48  
Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp  
150 155 160

CTT CTG CTG CTG GCA CTC GTG GTG CCC TCG GCC AGC GCC CAG GCC CTC 96  
Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu

165	170	175	180	
AGC TAC AGG GAG GCC GTG CTT CGT GCT GTG GAT CGC CTC AAC GAG CAG Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln 185		190	195	144
TCC TCG GAA GCT AAT CTC TAC CGC CTC CTG GAG CTG GAC CAG CCG CCC Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro 200	205		210	192
AAG GCC GAC GAG GAC CCG GGC ACC CCG AAA CCT GTG AGC TTC ACG GTG Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val 215	220	225		240
AAG GAG ACT GTG TGT CCC AGG CCG ACC CGG CAG CCC CCG GAG CTG TGT Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys 230	235	240		288
GAC TTC AAG GAG AAC GGG CGG GTG AAA CAG TGT GTG GGG ACA GTC ACC Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr 245	250	255	260	336
CTG GAT CAG ATC AAG GAC CCG CTC GAC ATC ACC TGC AAT GAG GTT CAA Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln 265	270		275	384
GGT GTC AGG GGA GGT GGC CTG TGC TAT TGT AGG CGT AGG TTC TGC GTC Gly Val Arg Gly Gly Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val 280	285	290		432
TGT GTC GGA CGA GGA TGA CGGTTGCGAC GGCAGGCTTT CCCTCCCCCA Cys Val Gly Arg Gly * 295				480
ATTTTCCCGG GGCCAGGTTT CCGTCCCCCA ATTTTCCGC CTCCACCTTT CCGGCCCGCA CCATTGGTC CACCAAGGTT CCCTGGTAGA CGGTGAAGGA TTTGCAGGCA ACTCACCCAG AAGGCCTTTC GGTACATTAA AATCCCAGCA AGGAGACCTA AGCATCTGCT TTGCCAGGC CCGCATCTGT CAAATAAATT CTTGTGAAAC C				540
				600
				660
				691

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Thr	Gln	Arg	Ala	Ser	Leu	Cys	Leu	Gly	Arg	Trp	Ser	Leu	Trp
1					5				10					15	

Leu	Leu	Leu	Leu	Ala	Leu	Val	Val	Pro	Ser	Ala	Ser	Ala	Gln	Ala	Leu
					20			25							30
Ser	Tyr	Arg	Glu	Ala	Val	Leu	Arg	Ala	Val	Asp	Arg	Leu	Asn	Glu	Gln
					35			40							45
Ser	Ser	Glu	Ala	Asn	Leu	Tyr	Arg	Leu	Glu	Leu	Asp	Gln	Pro	Pro	
					50			55							60
Lys	Ala	Asp	Glu	Asp	Pro	Gly	Thr	Pro	Lys	Pro	Val	Ser	Phe	Thr	Val
					65			70							80
Lys	Glu	Thr	Val	Cys	Pro	Arg	Pro	Thr	Arg	Gln	Pro	Pro	Glu	Leu	Cys
					85				90						95
Asp	Phe	Lys	Glu	Asn	Gly	Arg	Val	Lys	Gln	Cys	Val	Gly	Thr	Val	Thr
					100			105							110
Leu	Asp	Gln	Ile	Lys	Asp	Pro	Leu	Asp	Ile	Thr	Cys	Asn	Glu	Val	Gln
					115			120							125
Gly	Val	Arg	Gly	Gly	Gly	Leu	Cys	Tyr	Cys	Arg	Arg	Arg	Phe	Cys	Val
						130			135						140
Cys	Val	Gly	Arg	Gly	*										
					145			150							

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 691 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:  
      (A) NAME/KEY: CDS  
      (B) LOCATION: 1..450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG	48	
Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp		
155	160	165
CTT CTG CTG CTG GCA CTC GTG GTG CCC TCG GCC AGC GCC CAG GCC CTC	96	
Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu		
170	175	180
AGC TAC AGG GAG GCC GTG CTT CGT GCT GTG GAT CGC CTC AAC GAG CAG	144	
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln		
185	190	195

TCC TCG GAA GCT AAT CTC TAC CGC CTC CTG GAG CTG GAC CAG CCG CCC Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro	192
200 205 210	
AAG GCC GAC GAG GAC CCG GGC ACC CCG AAA CCT GTG AGC TTC ACG GTG Lys Ala Asp Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val	240
215 220 225 230	
AAG GAG ACT GTG TGT CCC AGG CCG ACC CGG CAG CCC CCG GAG CTG TGT Lys Glu Thr Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys	288
235 240 245	
GAC TTC AAG GAG AAC GGG CGG GTG AAA CAG TGT GTG GGG ACA GTC ACC Asp Phe Lys Glu Asn Gly Arg Val Lys Gln Cys Val Gly Thr Val Thr	336
250 255 260	
CTG GAT CAG ATC AAG GAC CCG CTC GAC ATC ACC TGC AAT GAG GTT CAA Leu Asp Gln Ile Lys Asp Pro Leu Asp Ile Thr Cys Asn Glu Val Gln	384
265 270 275	
GGT GTC AGG GGA GGT CGC CTG TGC TAT TGT AGG GGT TGG ATC TGC TTC Gly Val Arg Gly Arg Leu Cys Tyr Cys Arg Gly Trp Ile Cys Phe	432
280 285 290	
TGT GTC GGA CGA GGA TGA CGGTTGCGAC GGCAGGCTTT CCCTCCCCCA Cys Val Gly Arg Gly *	480
295 300	
ATTTTCCCGG GGCCAGGTTT CCGTCCCCCA ATTTTTCCGC CTCCACCTTT CCGGCCCGCA	540
CCATTGGTC CACCAAGGTT CCCTGGTAGA CGGTGAAGGA TTTGCAGGCA ACTCACCCAG	600
AAGGCCTTTC GGCACATTAA AATCCCAGCA AGGAGACCTA AGCATCTGCT TTGCCAGGC	660
CCGCATCTGT CAAATAAATT CTTGTGAAAC C	691

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp	
1 5 10 15	
Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu	
20 25 30	
Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln	
35 40 45	

Ser	Ser	Glu	Ala	Asn	Leu	Tyr	Arg	Leu	Leu	Glu	Leu	Asp	Gln	Pro	Pro
50					55					60					
Lys	Ala	Asp	Glu	Asp	Pro	Gly	Thr	Pro	Lys	Pro	Val	Ser	Phe	Thr	Val
65					70				75						80
Lys	Glu	Thr	Val	Cys	Pro	Arg	Pro	Thr	Arg	Gln	Pro	Pro	Glu	Leu	Cys
				85					90						95
Asp	Phe	Lys	Glu	Asn	Gly	Arg	Val	Lys	Gln	Cys	Val	Gly	Thr	Val	Thr
				100				105							110
Leu	Asp	Gln	Ile	Lys	Asp	Pro	Leu	Asp	Ile	Thr	Cys	Asn	Glu	Val	Gln
				115				120							125
Gly	Val	Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Cys	Arg	Gly	Trp	Ile	Cys	Phe
					130			135			140				
Cys	Val	Gly	Arg	Gly	*										
					145			150							

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1843 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: join(1..198, 603..710, 863..934, 1531..1602)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GAG ACC CAG AGA GCC AGC CTG TGC CTG GGG CGC TGG TCA CTG TGG Met Glu Thr Gln Arg Ala Ser Leu Cys Leu Gly Arg Trp Ser Leu Trp	48
1                   5                   10                   15	
 CTT CTG CTG CTG GCA CTC GTG GTG CCC TCG GCC AGC GCC CAG GCC CTC Leu Leu Leu Leu Ala Leu Val Val Pro Ser Ala Ser Ala Gln Ala Leu	96
20                   25                   30	
 AGC TAC AGG GAG GCC GTG CTT CGT GCT GTG GAT CGC CTC AAC GAG CAG Ser Tyr Arg Glu Ala Val Leu Arg Ala Val Asp Arg Leu Asn Glu Gln	144
35                   40                   45	
 TCC TCG GAA GCT AAT CTC TAC CGC CTC CTG GAG CTG GAC CAG CCG CCC Ser Ser Glu Ala Asn Leu Tyr Arg Leu Leu Glu Leu Asp Gln Pro Pro	192
50                   55                   60	
 AAG GCC GTGAGTCGGG CAGGGGCTCA GGAGGGGCTG GGGGGCGGGG GCTGTCCCCC	248

Lys Ala  
 65

ACCCGCCCG GGGCTCCCTG TCCCTCCCC TGCTCAGGCT GTCCCTCCTG CCAGGAAGGC	308
ACTTGTCCCT CTAAGGGGGA CCCCTCTGC CAGGAAACCT TCCCAGAGCT GGGTGCCCTG	368
CCCGCGTGAG AGCTTCCCAG CTTAGCCTCT GGGCTGTGGG CTCAGGGCCC TGCACAGCCT	428
GTGAGGCAGG AGCAGGCTCT GTCCCCCTCCC CTGTGCACCC AGCACCAAGC CCAGGGCCAG	488
GCTCCCAGCA GGGGCTGCAG AGGCTGCTGT CTAGGTGGGG GCAGGGAGGG GGTGACAGAT	548
CCGAGGGGGA AGCCTGAGCC CGAGTCCCAT CTCCCCACTT TGATCCTTGA CCAG GAC Asp	605
GAG GAC CCG GGC ACC CCG AAA CCT GTG AGC TTC ACG GTG AAG GAG ACT	653
Glu Asp Pro Gly Thr Pro Lys Pro Val Ser Phe Thr Val Lys Glu Thr	
70 75 80	
GTG TGT CCC AGG CCG ACC CGG CAG CCC CCG GAG CTG TGT GAC TTC AAG	701
Val Cys Pro Arg Pro Thr Arg Gln Pro Pro Glu Leu Cys Asp Phe Lys	
85 90 95	
GAG AAC GGG GTGAGGCTGG GGGCTGGGG CGCTGGCGGA TGCTTCCCAA	750
Glu Asn Gly	
100	
GGAGCTGAAC AGGAGAGCCT GCTGGGAAG ATGTCCAGGC CCTGGGTGA GGCTGGGAGC	810
TCATGGATGG AGGAGGGGG GTCCCAAGTTT GACCTTGAGT CTCCCCTTCC AG CGG Arg	865
GTG AAA CAG TGT GTG GGG ACA GTC ACC CTG GAT CAG ATC AAG GAC CCG	913
Val Lys Gln Cys Val Gly Thr Val Thr Leu Asp Gln Ile Lys Asp Pro	
105 110 115	
CTC GAC ATC ACC TGC AAT GAG GTGAGTGGCC CCTTATTGGT GTCAAGTTGC	964
Leu Asp Ile Thr Cys Asn Glu	
120 125	
TAATGGTTG GTGTGGGAA CTCTTGGGA GTGTTACCCG CTGCCCATC CAGGGCGTGG	1024
AAAGGCCCTC CTACCCGGC CCTTCCCTCA CCTCGGCCCC AGGGCTCCAG GTCTGGCTCT	1084
GTCATCCTTA GGGCCGCGGT TCCCTCAATG GGGTCCCCC CTCGTATTTG TCAGAAAGGC	1144
ACATTCAGG CCCCACCCCG ACCCTCTGAA TCACACTCTT GGGTGGAGCC CAGCCTTGTG	1204
TCTTCTCCCA AGATCCCAGC GGGTTCTTCC TGTGCTGTCG GCTGAGAGGC AGTGACCGGA	1264
CTAATGGACT TGCAGGCCCT GCTCCTGGCC AGCTTGCAG GGCTGGTTT GGGACCTGG	1324
CAAGGCCCCA GCCATCTCTG GGCCTGAGTC CACTTATGTG TCTGTGGGG ATTCCACCAC	1384

GTCGCTCCAAA	GGTCACAGGCC	AGAGGGTGGAC	CAGGGCCCCA	AGCCTCTTAC	TGTTTCCCCA	1444
TTCAGGGATT	TTTCTAGTCT	GGAGGGAGGG	TTCTTGTCTT	GACCCTGGC	CAGACCCCAC	1504
CCGAAACCTG	TTTCTCTTGG	TCACAG	GTT CAA GGT GTC AGG GGA GGT CGC CTG			1557
			Val Gln Gly Val Arg Gly Gly Arg Leu			
			130		135	
TGC TAT TGT AGG CGT AGG TTC TGC GTC TGT GTC GGA CGA GGA TGA						1602
Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val Gly Arg Gly *						
140	145	150				
CGGTTGCGAC	GGCAGGCTTT	CCCTCCCCA	ATTTTCCCGG	GGCCAGGTTT	CCGTCCCCA	1662
ATTTTTCCGC	CTCCACCTTT	CCGGCCCGCA	CCATTGGTC	CACCAAGGTT	CCCTGGTAGA	1722
CGGTGAAGGA	TTTGCAGGCA	ACTCACCCAG	AAGGCCTTTC	GGTACATTAA	AATCCCAGCA	1782
AGGAGACCTA	AGCATCTGCT	TTGCCAGGC	CCGCATCTGT	CAAATAAATT	CTTGTGAAAC	1842
C						1843

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 150 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Glu	Thr	Gln	Arg	Ala	Ser	Leu	Cys	Leu	Gly	Arg	Trp	Ser	Leu	Trp
1				5						10				15	
Leu	Leu	Leu	Leu	Ala	Leu	Val	Val	Pro	Ser	Ala	Ser	Ala	Gln	Ala	Leu
					20				25					30	
Ser	Tyr	Arg	Glu	Ala	Val	Leu	Arg	Ala	Val	Asp	Arg	Leu	Asn	Glu	Gln
						35			40					45	
Ser	Ser	Glu	Ala	Asn	Leu	Tyr	Arg	Leu	Leu	Glu	Leu	Asp	Gln	Pro	Pro
						50			55					60	
Lys	Ala	Asp	Glu	Asp	Pro	Gly	Thr	Pro	Lys	Pro	Val	Ser	Phe	Thr	Val
						65			70					75	
Lys	Glu	Thr	Val	Cys	Pro	Arg	Pro	Thr	Arg	Gln	Pro	Pro	Glu	Leu	Cys
						85			90					95	
Asp	Phe	Lys	Glu	Asn	Gly	Arg	Val	Lys	Gln	Cys	Val	Gly	Thr	Val	Thr
							100			105				110	
Leu	Asp	Gln	Ile	Lys	Asp	Pro	Leu	Asp	Ile	Thr	Cys	Asn	Glu	Val	Gln

115

120

125

Gly Val Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val  
130 135 140

Cys Val Gly Arg Gly \*  
145 150

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 4..13

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 6..11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Ile Cys Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Arg Gly Gly Gly Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val  
1                   5                   10                   15  
  
Gly Arg

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Gly Trp Ile Cys Phe Cys Val  
1                   5                   10                   15  
  
Gly Arg

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Phe Phe Arg Leu Cys Tyr Cys Arg Pro Arg Phe Cys Val Cys Val  
1                   5                   10                   15  
  
Gly Arg

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Cys	Arg	Arg	Arg	Phe	Cys	Val	Cys	Val
1				5				10						15	
Gly Arg															

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Cys	Arg	Arg	Arg	Phe	Cys	Ile	Cys	Val
1					5			10					15		

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg	Gly	Gly	Gly	Leu	Cys	Tyr	Cys	Arg	Arg	Arg	Phe	Cys	Val	Cys	Val
1					5			10					15		
Gly Arg															

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Cys	Arg	Gly	Trp	Ile	Cys	Phe	Cys	Val
1				5						10					15
Gly Arg															

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Cys	Arg	Pro	Arg	Phe	Cys	Val	Cys	Val
1					5					10					15
Gly Arg															

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 4  
(D) OTHER INFORMATION: /product= "homoarginine(Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Arg Gly Gly Xaa Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: group(4, 9)  
(D) OTHER INFORMATION: /product= "homoarginine(Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Arg Gly Gly Xaa Leu Cys Tyr Cys Xaa Arg Arg Phe Cys Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 10  
(D) OTHER INFORMATION: /product= "homoarginine(Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Arg Gly Gly Arg Val Cys Tyr Cys Arg Xaa Arg Phe Cys Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Lys Lys Trp Cys Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine (Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Xaa Arg Tyr Cys Val Cys Val  
1                       5                           10                           15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Arg Gly Ser Gly Leu Cys Tyr Cys Arg Arg Lys Trp Cys Val Cys Val  
1                       5                           10                           15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Arg Ala Thr Arg Ile Cys Phe Cys Arg Arg Arg Phe Cys Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine(Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg Gly Gly Lys Val Cys Tyr Cys Arg Xaa Arg Phe Cys Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "D-form of amino acid"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "D form of amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Arg Ala Thr Arg Ile Cys Phe Cys Arg Arg Arg Phe Cys Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine (Har)"  
/note= "D form of amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Arg Gly Gly Lys Val Cys Tyr Cys Arg Xaa Arg Phe Cys Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "All D-form amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
- (A) NAME/KEY: Region
  - (B) LOCATION: 1..16
  - (D) OTHER INFORMATION: /note= "All D-form amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Ile Cys Val  
1                       5                           10                           15

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
- (A) NAME/KEY: Region
  - (B) LOCATION: 1..18
  - (D) OTHER INFORMATION: /note= "All D-form amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Gly Gly Gly Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val  
1                       5                           10                           15  
  
Gly Arg

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
- (A) NAME/KEY: Region

(B) LOCATION: 1..18  
(D) OTHER INFORMATION: /note= "All D-form amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Gly Trp Ile Cys Phe Cys Val  
1 5 10 15  
Gly Arg

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg Gly Gly Arg Leu Val Tyr Cys Arg Arg Arg Phe Cys Val Cys Val  
1 5 10 15  
Gly Arg

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Gly Gly Arg Leu Gly Tyr Cys Arg Arg Arg Phe Cys Ile Cys Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY. linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Arg Gly Gly Gly Leu Cys Tyr Gly Arg Arg Arg Phe Cys Val Cys Val  
1 5 10 15  
Gly Arg

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Arg Gly Gly Arg Leu Gly Tyr Gly Arg Arg Arg Phe Gly Val Cys Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Lys Gly Gly Arg Leu Val Tyr Val Arg Arg Arg Phe Ile Val Cys Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "homoarginine (Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Arg Gly Gly Xaa Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Gly Val  
1                       5                           10                           15

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(4, 9)
- (D) OTHER INFORMATION: /product= "homoarginine (Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Arg Gly Gly Xaa Leu Cys Tyr Cys Xaa Arg Arg Phe Cys Val Leu Val  
1                       5                           10                           15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine (Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Arg Gly Gly Arg Val Cys Tyr Val Arg Xaa Arg Phe Leu Val Gly Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Gly Gly Arg Leu Cys Tyr Ser Arg Lys Lys Trp Cys Val Ser Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine(Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Xaa Arg Tyr Ser Val Val Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Arg Gly Ser Gly Leu Ser Tyr Cys Arg Arg Lys Trp Gly Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Arg Ala Thr Arg Ile Ser Phe Ser Arg Arg Arg Phe Ser Val Ser Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine (Har)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Arg Gly Gly Lys Val Cys Tyr Gly Arg Xaa Arg Phe Ser Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(9, 18)
- (D) OTHER INFORMATION: /note= "D form of amino acids"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Arg Ala Thr Arg Ile Val Phe Cys Arg Arg Arg Phe Gly Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "homoarginine(Har)"  
/note= "D form of amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg Gly Gly Lys Val Cys Tyr Leu Arg Xaa Arg Phe Leu Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Arg Gly Gly Arg Ile Cys Phe Leu Arg Pro Arg Ile Gly Val Cys Val  
1               5                   10                   15  
  
Gly Arg

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 8..13

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Arg Gly Gly Arg Leu Xaa Tyr Cys Arg Arg Arg Phe Cys Val Xaa Val  
1               5                   10                   15  
  
Gly Arg

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Disulfide-bond  
(B) LOCATION: 8..13

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: group(6, 15)  
(D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Arg Gly Gly Arg Leu Xaa Tyr Cys Arg Arg Arg Phe Cys Ile Xaa Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Disulfide-bond  
(B) LOCATION: 8..13

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: group(6, 15)  
(D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Arg Gly Gly Gly Leu Xaa Tyr Cys Arg Arg Arg Phe Cys Val Xaa Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: Disulfide-bond  
(B) LOCATION: 8..13

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: group(6, 15)  
(D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Arg	Gly	Gly	Arg	Leu	Xaa	Tyr	Cys	Arg	Trp	Gly	Ile	Cys	Phe	Xaa	Val
1				5						10					15
Gly Arg															

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: Disulfide-bond  
(B) LOCATION: 8..13

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: group(6, 15)  
(D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Arg	Gly	Gly	Arg	Leu	Xaa	Tyr	Cys	Arg	Pro	Arg	Phe	Cys	Val	Xaa	Val
1				5					10						15
Gly Arg															

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: Disulfide-bond  
(B) LOCATION: 6..15

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: group(8, 13)  
(D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Xaa	Arg	Arg	Arg	Phe	Xaa	Val	Cys	Val
1				5				10						15	
Gly Arg															

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: Disulfide-bond  
(B) LOCATION: 6..15

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: group(8, 13)  
(D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Arg	Gly	Gly	Arg	Leu	Cys	Tyr	Xaa	Arg	Arg	Arg	Phe	Xaa	Ile	Cys	Val
1					5				10					15	
Gly Arg															

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Disulfide-bond
- (B) LOCATION: 6..15

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(8, 13)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg Gly Gly Arg Leu Cys Tyr Xaa Arg Pro Arg Phe Xaa Val Cys Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 8, 13, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Arg Gly Gly Arg Leu Xaa Tyr Xaa Arg Arg Arg Phe Xaa Val Xaa Val  
1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 8, 13, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Arg Gly Gly Arg Leu Xaa Tyr Xaa Arg Arg Arg Phe Xaa Ile Xaa Val  
1               5                           10                           15

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(6, 8, 13, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Arg Gly Gly Gly Leu Xaa Tyr Xaa Arg Arg Arg Phe Xaa Val Xaa Val  
1               5                           10                           15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(5, 7, 13, 15)
- (D) OTHER INFORMATION: /note= "X is a hydrophobic, a small, or a large polar amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTCGTCTAGA SGTTTCACAA GAATTATTT

30

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Gly Trp Ile Cys Phe Cys Val  
1 5 10 15

Gly Arg Gly

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGGCCGTGA GTCG

14

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AACGGGGTGA GGCT

14

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AATGAGGTGA GTGG

14

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTGACCAGGA CGAG

14

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCTTCCAGCG GGTG

14

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGTCACAGGT TCAA

14